

THE LANCET Infectious Diseases

Supplementary webappendix

This webappendix formed part of the original submission and has been peer reviewed.
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Supplement to: Faye O, Pratt CB, Faye M, et al. Genomic characterisation of human monkeypox virus in Nigeria. *Lancet Infect Dis* 2018; published online Jan 16.
[http://dx.doi.org/10.1016/S1473-3099\(18\)30043-4](http://dx.doi.org/10.1016/S1473-3099(18)30043-4).

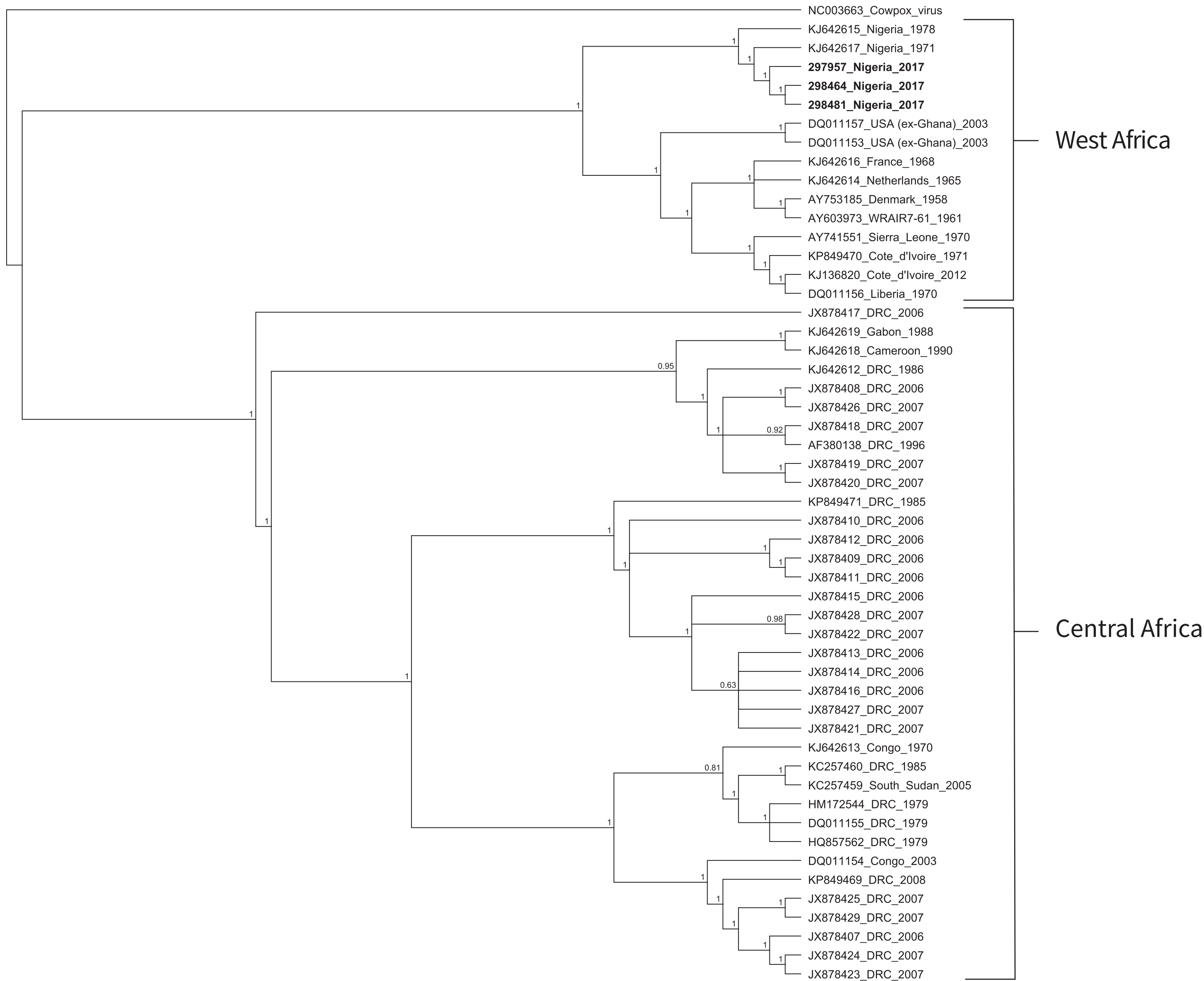


Figure: Phylogenetic tree produced from three isolate draft consensus sequences and 48 archived MPXV complete sequences from GenBank, rooted with the cowpox virus reference sequence NC_003363, using MrBayes 3.2.6^{1,2} with 1 000 000 generations and sampling every 200. Posterior probabilities are indicated at each node. Central and west African clades are indicated. The outbreak consensus sequences align most closely to sequences of Nigerian origin.

1 Katoh K, Standley DM. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol* 2013; **30**: 772–80.

2 Huelsenbeck JP, Ronquist F. MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics* 2001; **17**: 754–55.